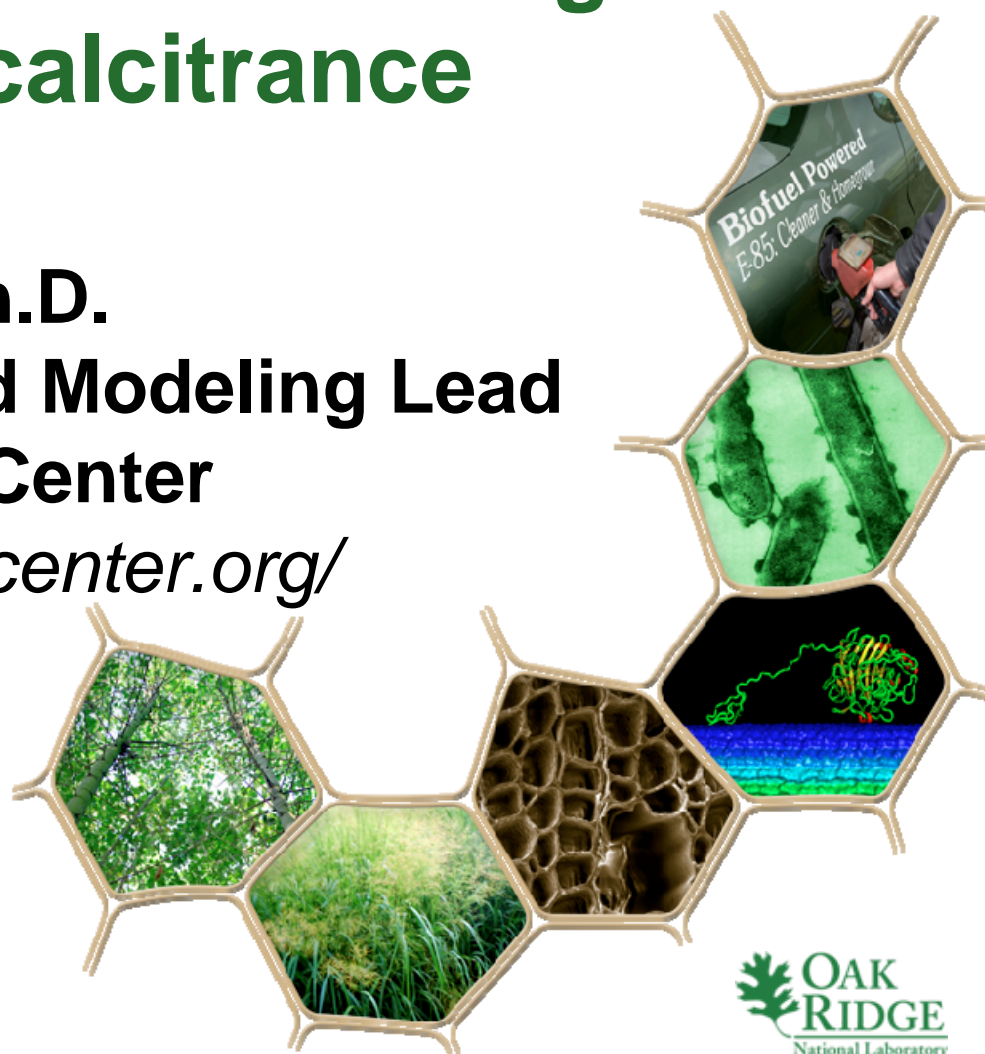


# The BioEnergy Science Center: Initial Results in Overcoming Biomass Recalcitrance

**Brian H. Davison, Ph.D.**  
**Characterization and Modeling Lead**  
**BioEnergy Science Center**

*<http://www.bioenergycenter.org/>*

*Biomass 2009*  
**March 17, 2009**

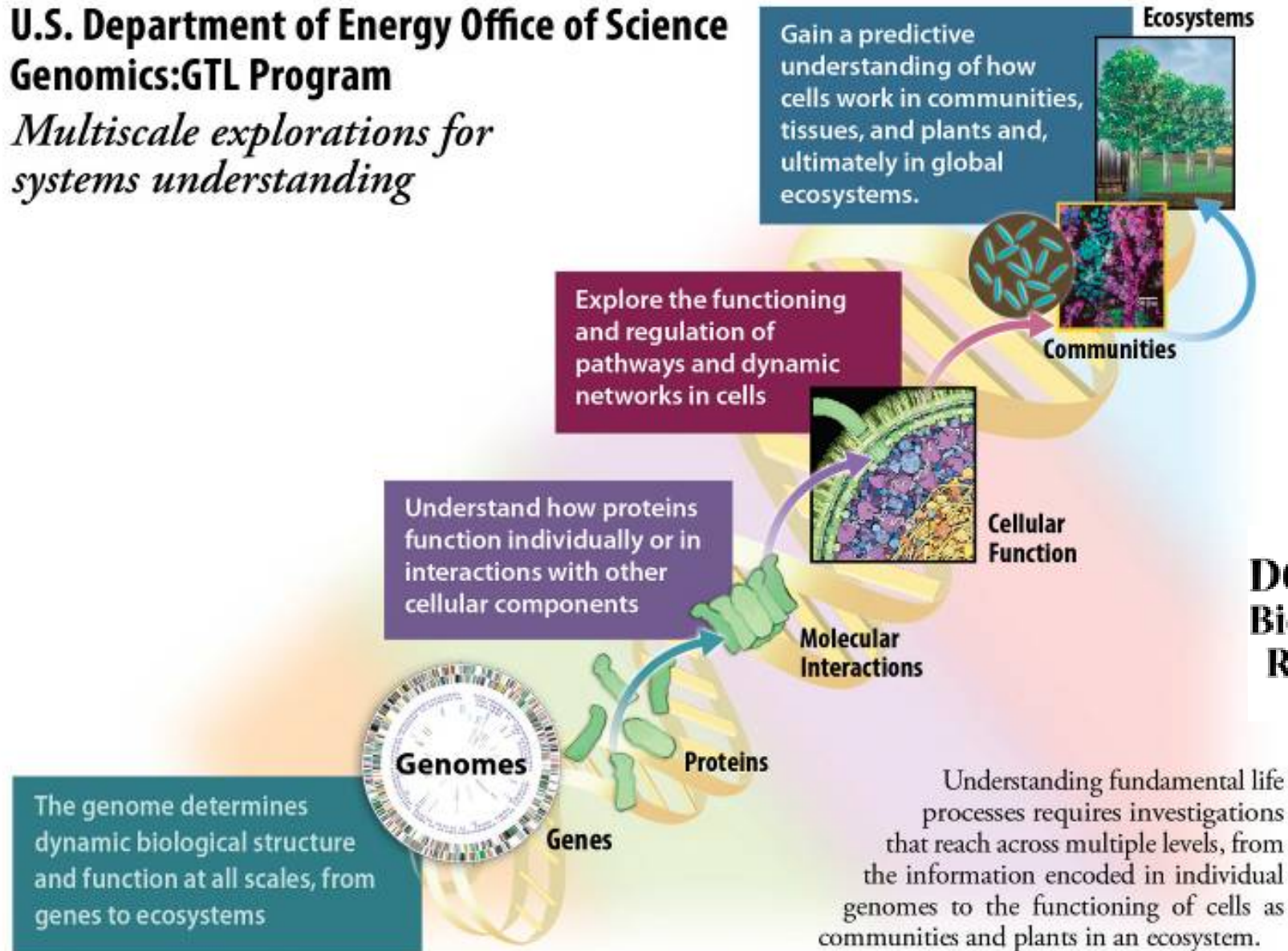


# GTL Core Science Goals at All Scales



## U.S. Department of Energy Office of Science Genomics:GTL Program

*Multiscale explorations for  
systems understanding*



DOE  
Bioenergy  
Research  
Centers

BESC  
y Science Center



# DOE-GTL Mission Challenges for Biology



**DOE**  
**Bioenergy**  
**Research**  
**Centers**



## Biofuels

**Gain knowledge and tools for using microbes and plants to build a national biofuel capability to**

- Develop sustainable energy crops.
- Develop biotechnologies for producing advanced biofuels

## Cleanup

**Understand microbial and plant impacts on subsurface contaminant fate to**

- Develop better assessment tools.
- Design improved bioremediation methodologies.

## Climate Stabilization

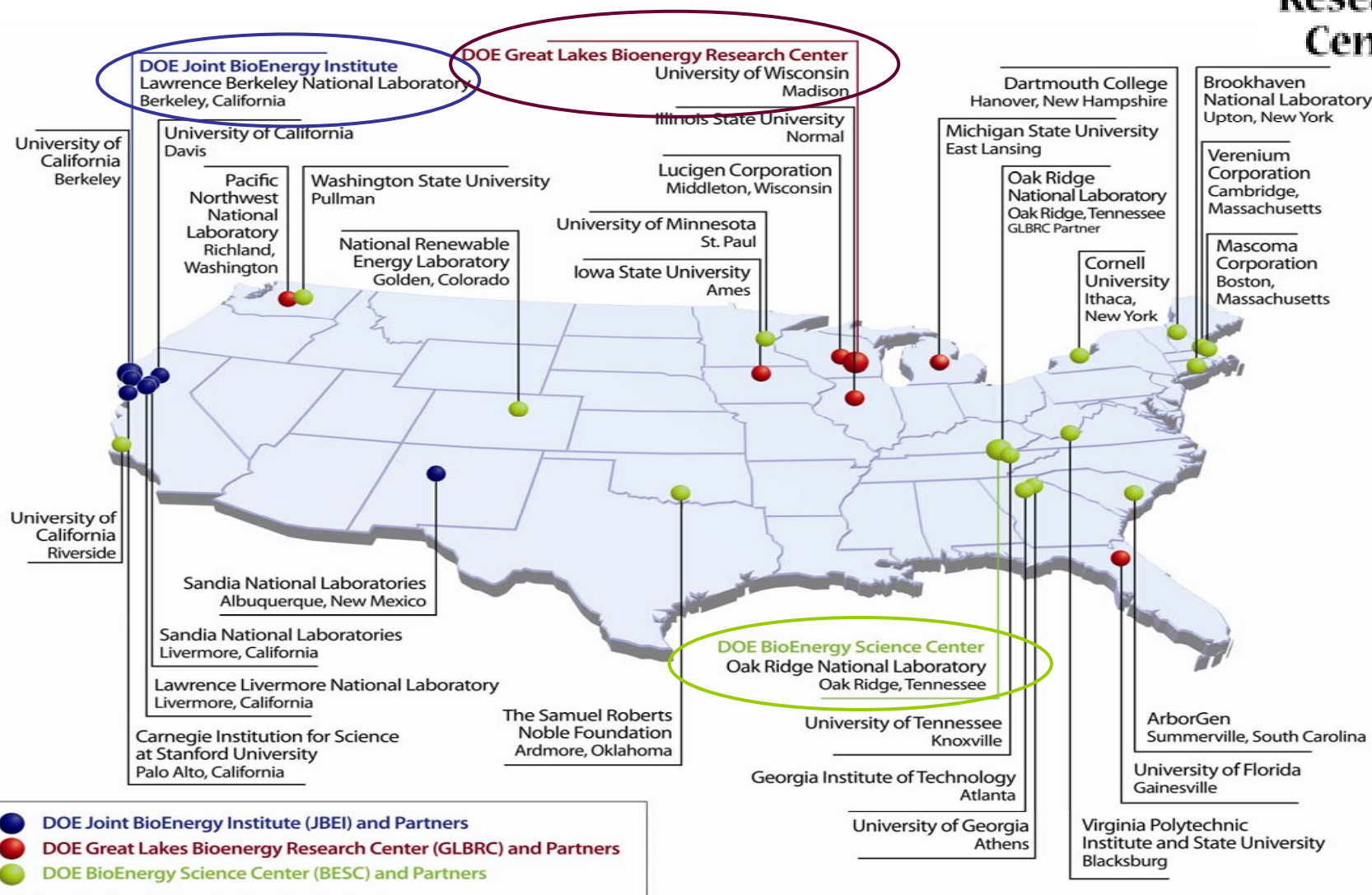
**Determine ocean and terrestrial ecosystems' contributions to the global carbon cycle to**

- Improve projections of climate change and its impacts.
- Create carbon-biosequestration strategies.

# DOE Bioenergy Research Centers: Multi-Institutional Partnerships



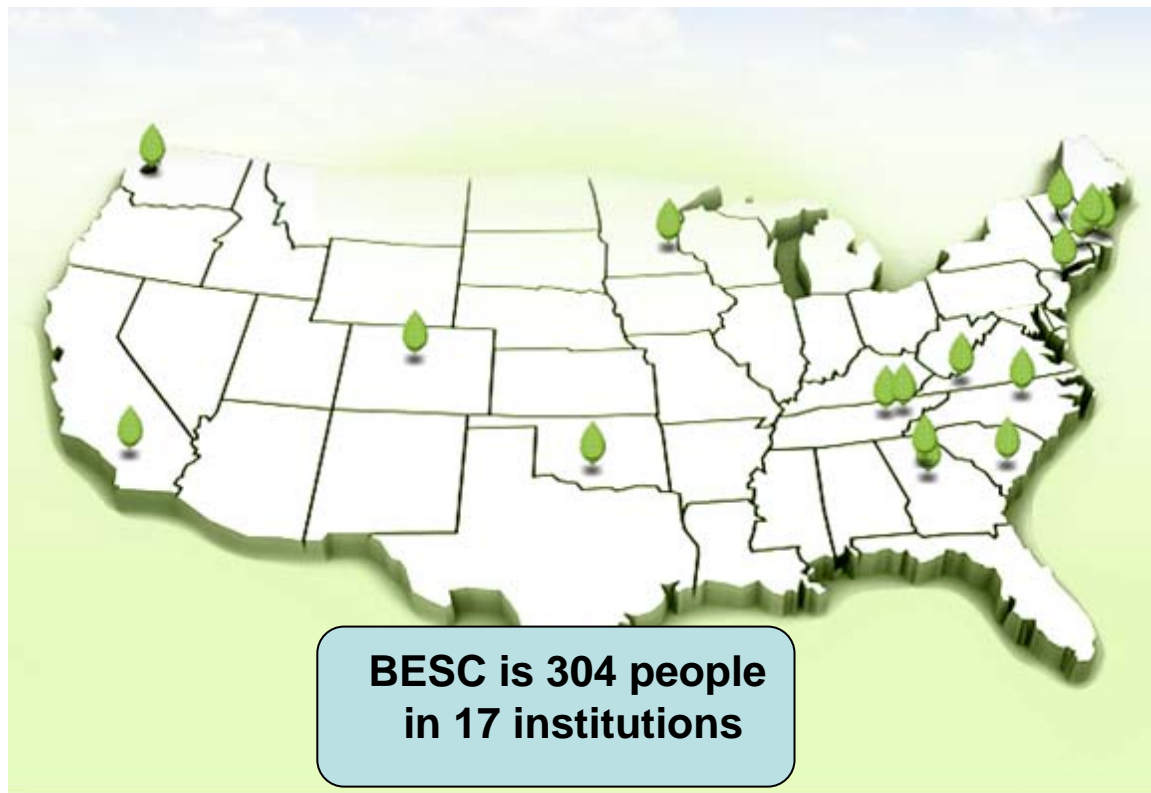
**DOE**  
**Bioenergy**  
**Research**  
**Centers**



# The BioEnergy Science Center



**BESC:** A multi-institutional DOE-funded center dedicated to understanding and modifying plant biomass recalcitrance

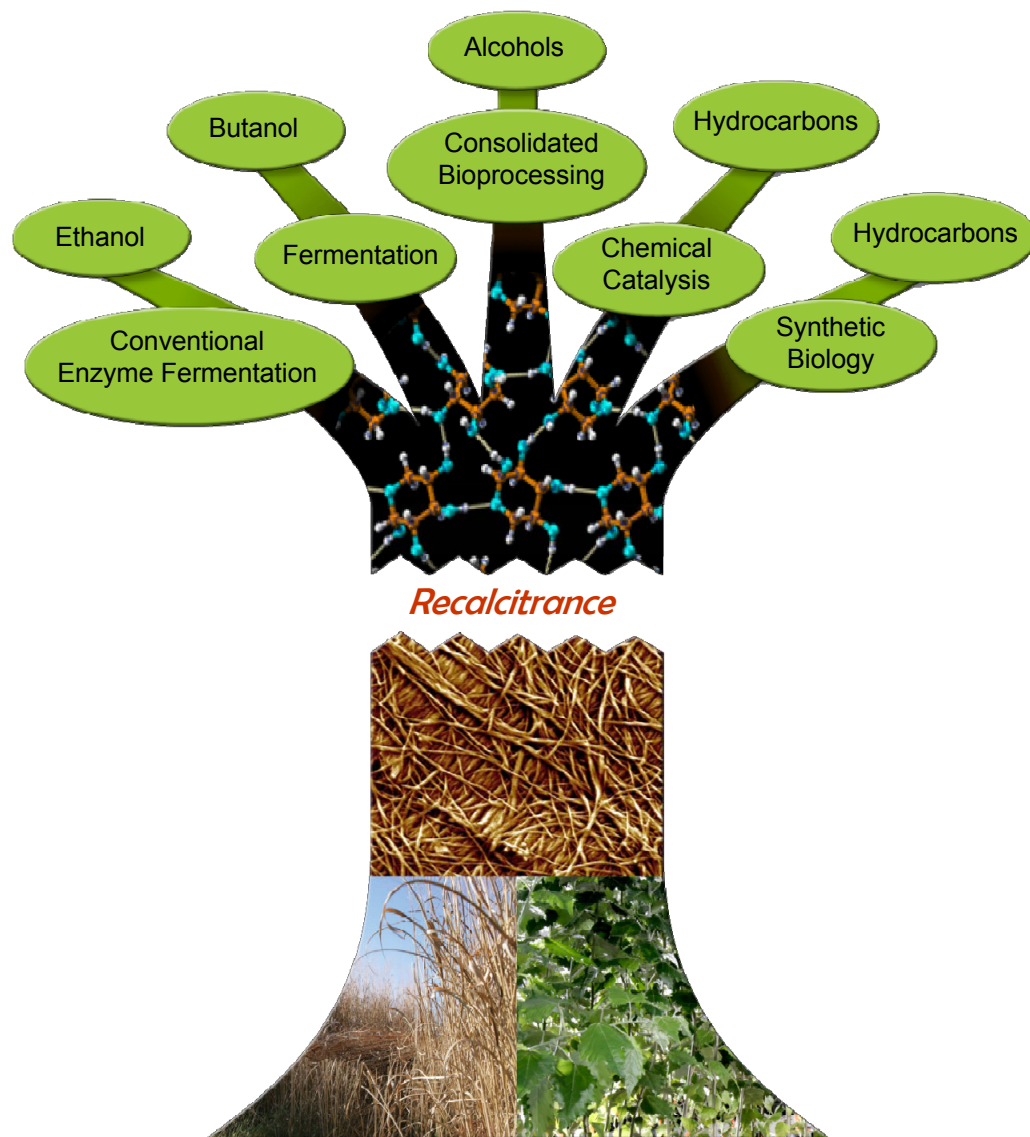


- Oak Ridge National Laboratory
- University of Georgia
- University of Tennessee
- National Renewable Energy Laboratory
- Georgia Institute of Technology
- Samuel Roberts Noble Foundation
- Dartmouth College
- ArborGen, LLC
- Verenium Corporation
- Mascoma Corporation
- University of California-Riverside
- Cornell University
- Washington State University
- University of Minnesota
- North Carolina State University
- Brookhaven National Laboratory
- Virginia Polytechnic Institute

<http://www.bioenergycenter.org/>



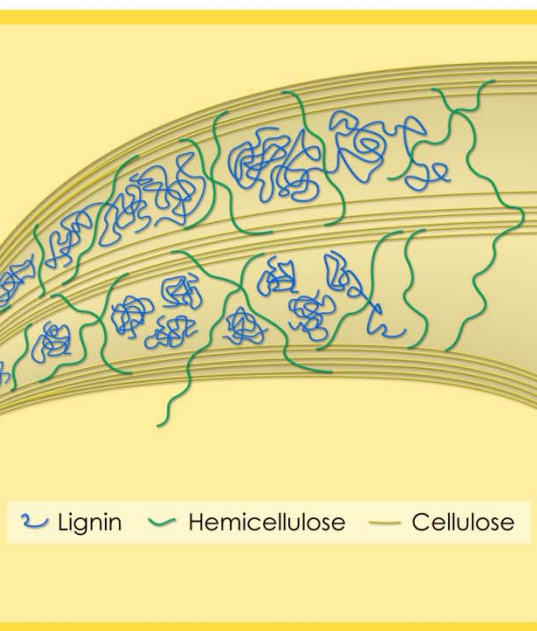
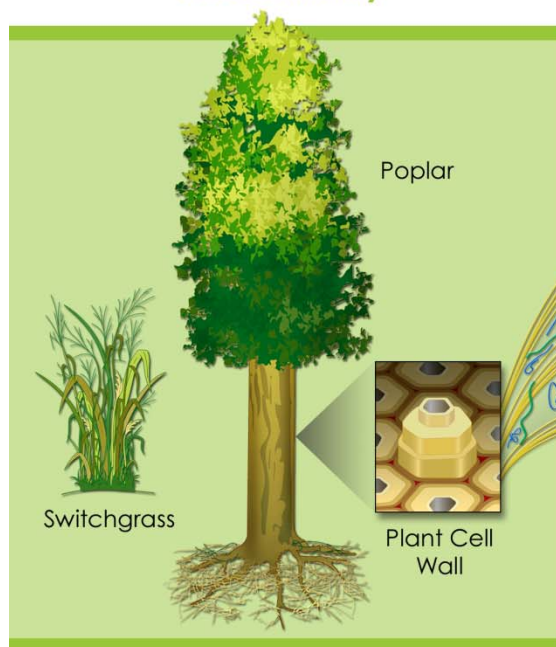
# Access to the Sugars in Lignocellulosic Biomass is the Current Critical Barrier



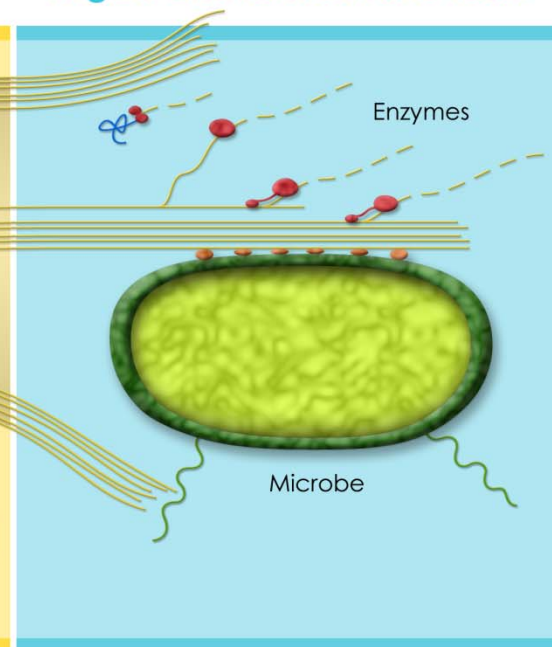
- Solving this will cut processing costs significantly and be used in most conversion processes
- This requires an integrated multidisciplinary approach
- Timeframe
  - Modified plants to field trials: Year 5
  - New or improved microbes to development: Years 4–5
  - Analysis and screening technologies: Year 3 on

# A Two-pronged Approach to Increase the Accessibility of Biomass Sugars

Modify the plant cell wall structure to increase accessibility

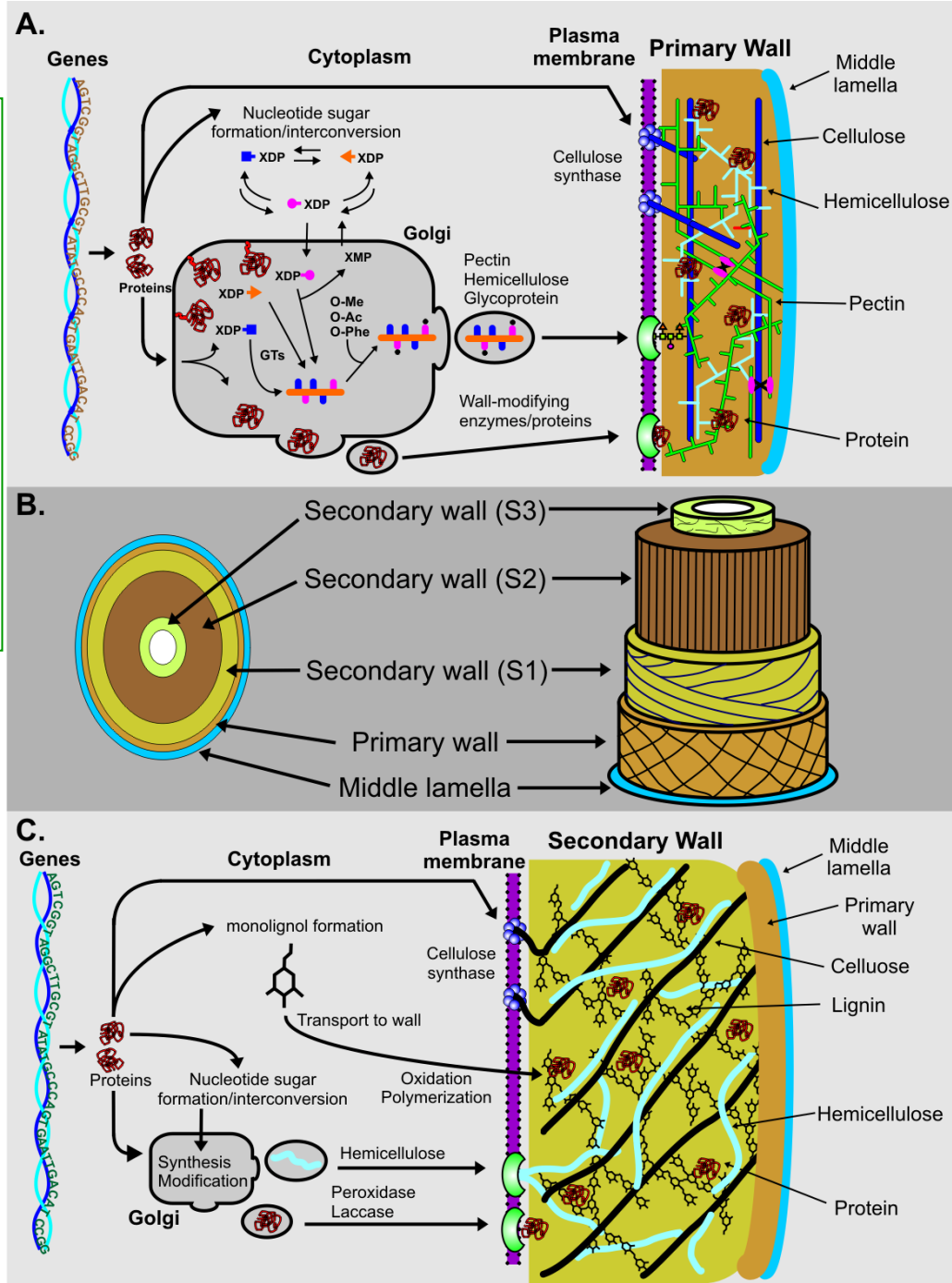


Improve combined microbial approaches that release sugars and ferment into fuels



Both utilize rapid screening for relevant traits followed by detailed analysis of selected samples

**Functional modifications of both primary and secondary cell walls may decrease recalcitrance**



**Primary Wall**  
90% polysaccharide

**Dividing and growing cells**

**Pectin  
Hemicellulose  
Cellulose  
(proteins)**

**Secondary Walls**  
70 – 80% polysaccharide

**Some cells with structural roles**

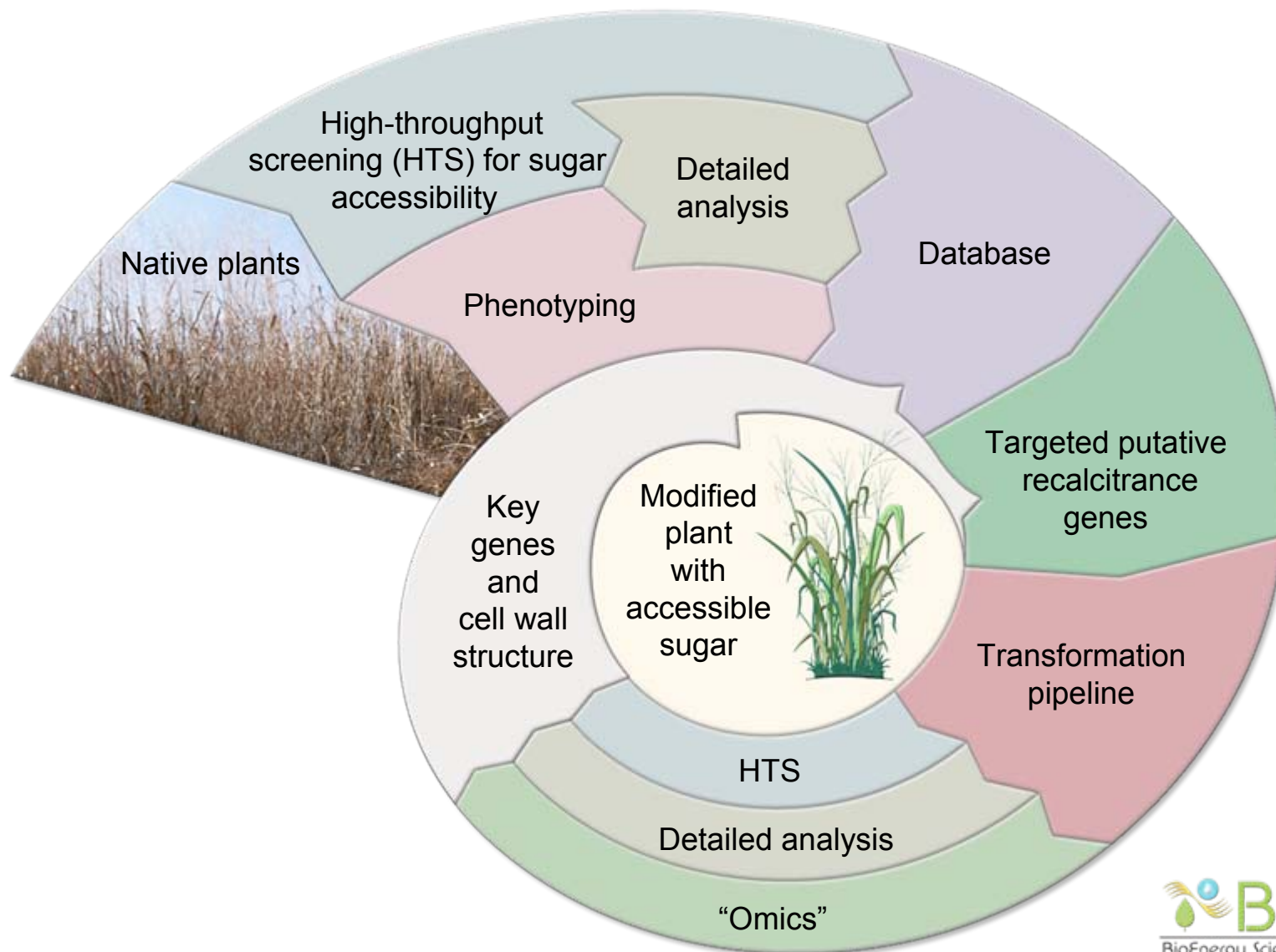
↓ **Pectin  
Hemicellulose  
Cellulose  
Lignin  
(proteins)**



Malcolm O'Neill, CCRC  
Mohnen et al. (2008)



# What Genes Control Cell Wall Synthesis (and Access to the Sugars)?



# Targeted Plant Genes and Transformation Pipeline

## Functions of initial targets (set #1)

Functional category	# genes
Cell wall biosynthesis	50
Cell division and expansion	46
Signal transduction	26
Stress response	20
Metabolism	19
Intracellular traffic	9
Protein fate	9
Transcription	9
Plant defence	4
Nucleic acid or nucleotide binding	2
Transporters	2
<b>Total</b>	<b>196</b>

- Gene transformation pipeline established and running
  - 70 *Populus* genes per set
  - 4 Switchgrass for stable transformation per set
  - 30 Switchgrass by VIGS (viral induced gene silencing) per set
  - Three sets totaling >300 genes in pipeline after three rounds of review
- *Populus*
  - Transformation: 200 genes per year
  - Activation Tagging: 1000 genes per year
- Switchgrass
  - Transformation: 20 genes Year 1; 40-60 Year 2
  - VIGS: 200 genes per year, RNAi
- Higher perennial plants have fewer genetic tools and so targets must be selected carefully



KnowledgeBase beta

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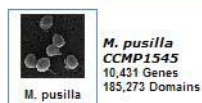
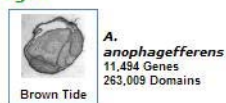
## BESC Plant Biomass Recalcitrance Genes

The Plant Biomass Recalcitrance Genes (PBRG) knowledge domain provides information on plant reference genomes, comparative gene annotation and integration of gene function information, plant gene transformation data, and plant cell wall biosynthesis pathways and other cell systems, with links to expression and other experimental studies.

### Plants



### Algae



### Others



★ [Transformation Pipeline Gene List](#)

Parang, Uberbacher et al.,

### •Reference Genomes

### \* BESC Curation

### \* Gene Discovery Tools

### \* Pathway building

### \*Links to BESC data

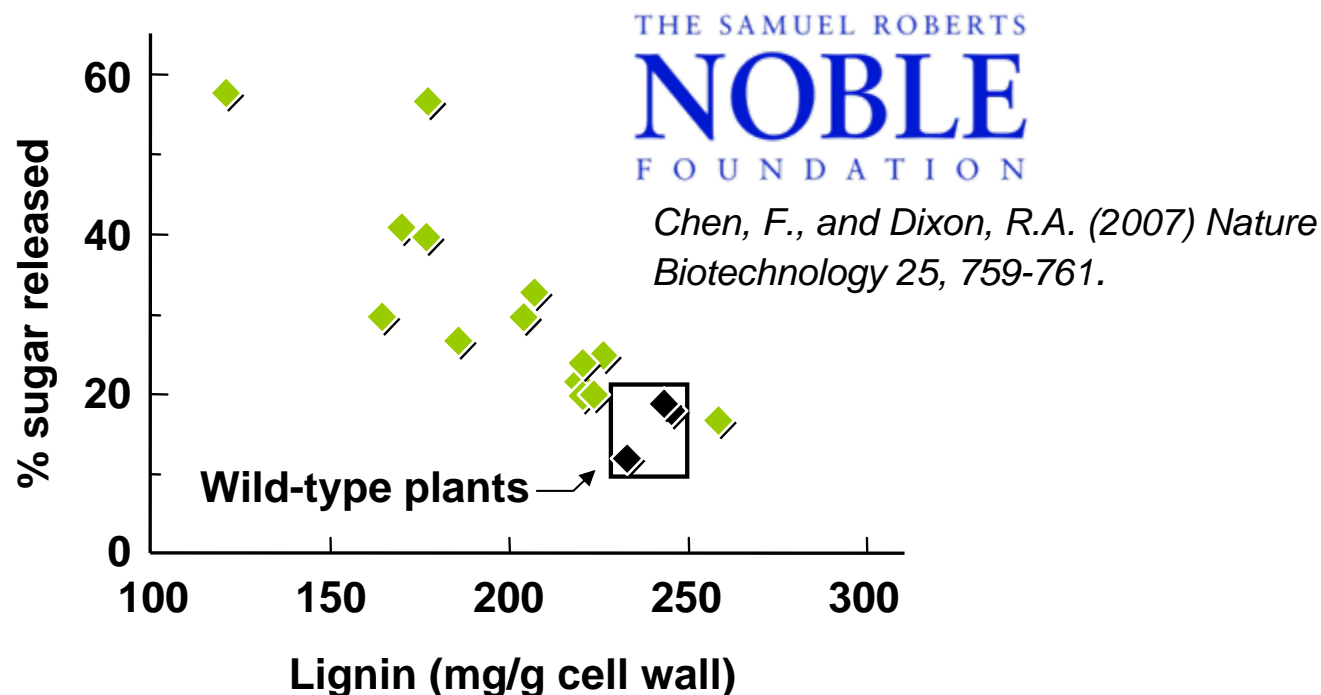
### Links to LIMS system



# *Targeted Cell Wall Synthesis*

## *Approach: A Few Examples*

# Modifying Cell Wall Composition and Structure Can Reduce Recalcitrance



- More sugar is solubilized by cellulase when the lignin content of alfalfa cell walls is reduced
- Strategy is feasible for *Populus* and switchgrass

# ***Discovery-based Approach* to Identify Recalcitrance-Associated Genes via Analysis of Natural Variation**



# Mining Genetic Variation in Switchgrass

Create diverse population  
by cross “lowland” SG AP-13  
and “upland” SG VS-16  
into 385 pseudo F1 clones



Pseudo F<sub>1</sub> population  
of 385 genotypes

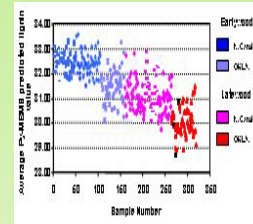


Clones ready for field planting

## HTS Pipeline



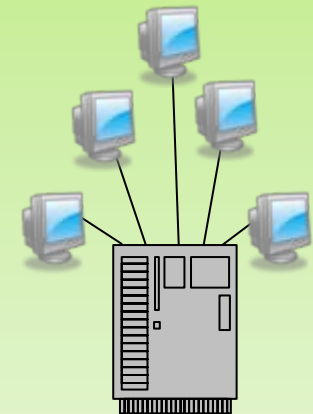
Sugar Release  
Assay



Analytical  
Pyrolysis

Create Genetic Marker Map  
to identify allelic variation

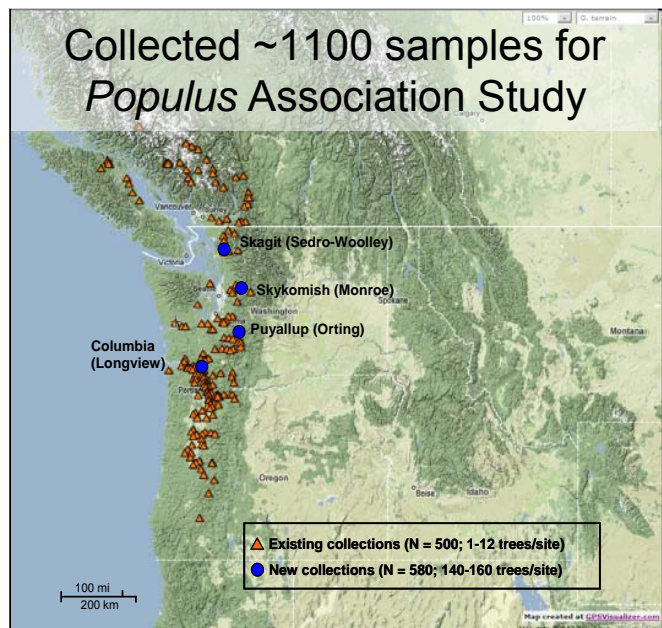
Identify Marker  
Trait Association



Cell Wall  
Biosynthesis  
Database



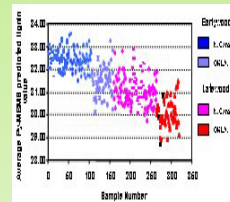
# Mining Variation to Identify Key Genes in Biomass Composition and Sugar Release



## HTS Pipeline



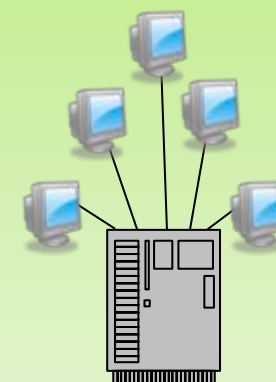
Sugar Release  
Assay



Analytical  
Pyrolysis

Create Genetic Marker Map  
to identify allelic variation

Identify Marker  
Trait Association



Cell Wall  
Biosynthesis  
Database



Establish common  
gardens for association  
and activation tag  
populations with 1000s  
of plants

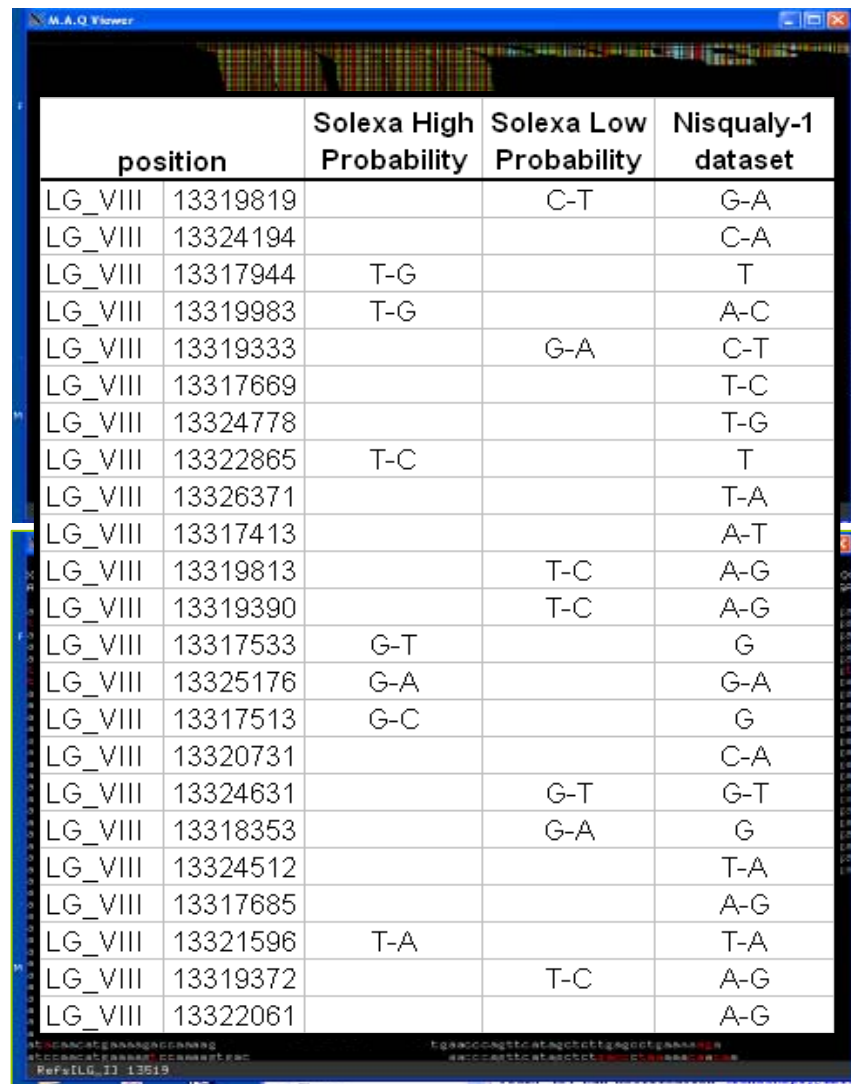
# Association Genetics Study – Whole-genome Resequencing in effort to discover SNPs across *Populus* genome

In collaboration with the Joint  
Genome Institute 10 alternate  
*Populus* genomes are being  
resequencing



## Preliminary Results

- 28x depth from 6 Solexa runs
- 85% align to Nisqually-1
- 843,000 SNP loci relative to reference
- 78,000 SNP loci are heterozygous



	position	Solexa High Probability	Solexa Low Probability	Nisqually-1 dataset
LG_VIII	13319819		C-T	G-A
LG_VIII	13324194			C-A
LG_VIII	13317944	T-G		T
LG_VIII	13319983	T-G		A-C
LG_VIII	13319333		G-A	C-T
LG_VIII	13317669			T-C
LG_VIII	13324778			T-G
LG_VIII	13322865	T-C		T
LG_VIII	13326371			T-A
LG_VIII	13317413			A-T
LG_VIII	13319813		T-C	A-G
LG_VIII	13319390		T-C	A-G
LG_VIII	13317533	G-T		G
LG_VIII	13325176	G-A		G-A
LG_VIII	13317513	G-C		G
LG_VIII	13320731			C-A
LG_VIII	13324631		G-T	G-T
LG_VIII	13318353		G-A	G
LG_VIII	13324512			T-A
LG_VIII	13317685			A-G
LG_VIII	13321596	T-A		T-A
LG_VIII	13319372		T-C	A-G
LG_VIII	13322061			A-G



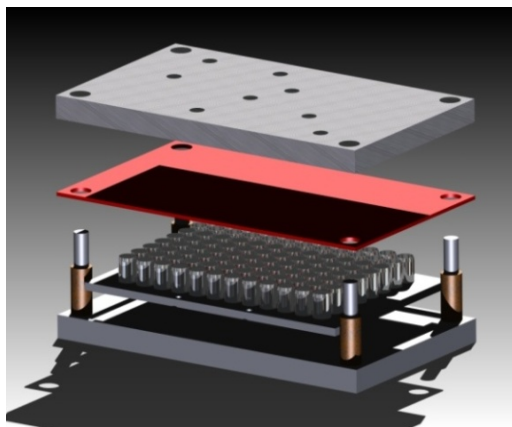
# HTP Characterization Pipeline for the Recalcitrance Phenotype

- Screening of 1000's of samples

Composition analytical  
pyrolysis, IR, confirmed by  
wet chemistry

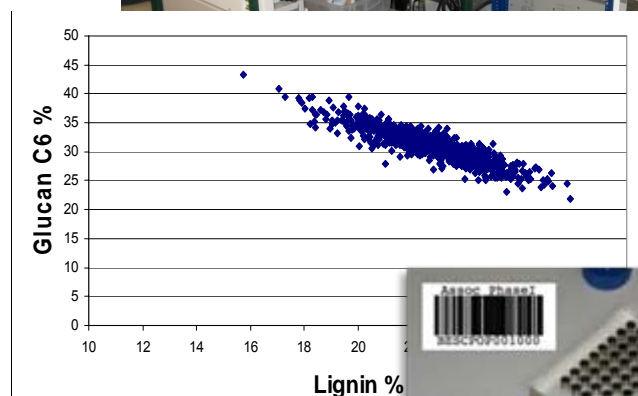
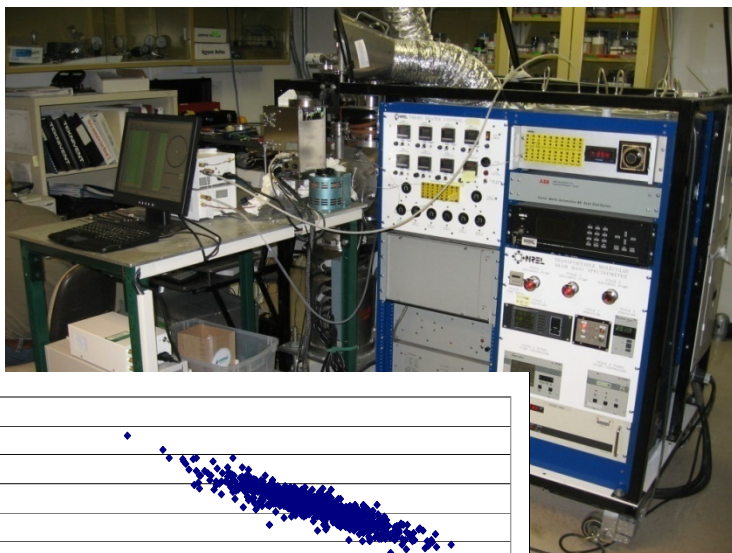
Pre-treatment  
new method with  
dilute acid and steam

Enzyme digestibility  
sugar release  
with enzyme cocktail



Detailed chemical and structural analyses of specific samples

# Composition Data from Analytic Pyrolysis (MBMS) for High-throughput Screening of Transgenic Populations

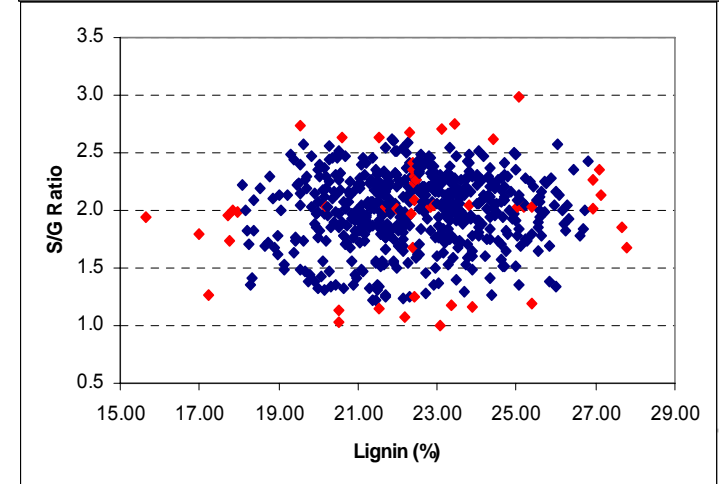
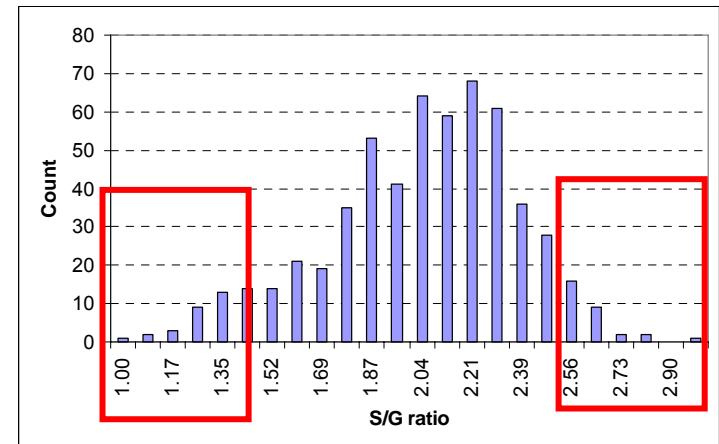
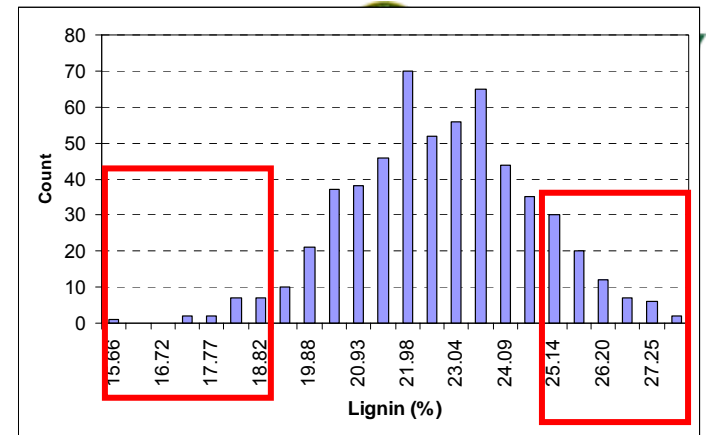


- Rapid (50/h w/ 4mg)
- Reliable
- Gives values for glucan, xylan, lignin, and details on monomers – e.g., S/G
- Complements time-consuming and more variable wet chemistry, molecular and biochemical analyses

Composition data from *Populus* association study (798 samples) represents full range of known *Populus* variation

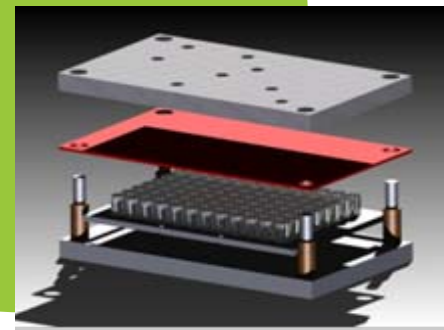
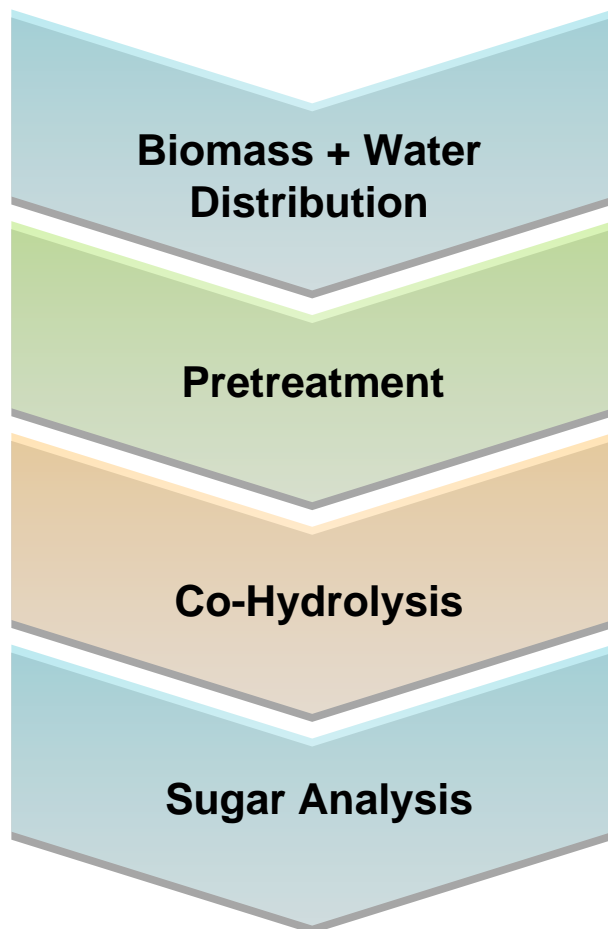
# Composition Data from *Populus* Association Study

- The association samples display extreme variation in lignin, S/G ratio, and sugar content
- There is a negative correlation between sugar content and lignin content
- All sampled genotypes are being replicated and will be established in a common garden experiment





# Enabling Technology: An HTP Pretreatment for 1000s of Small Samples

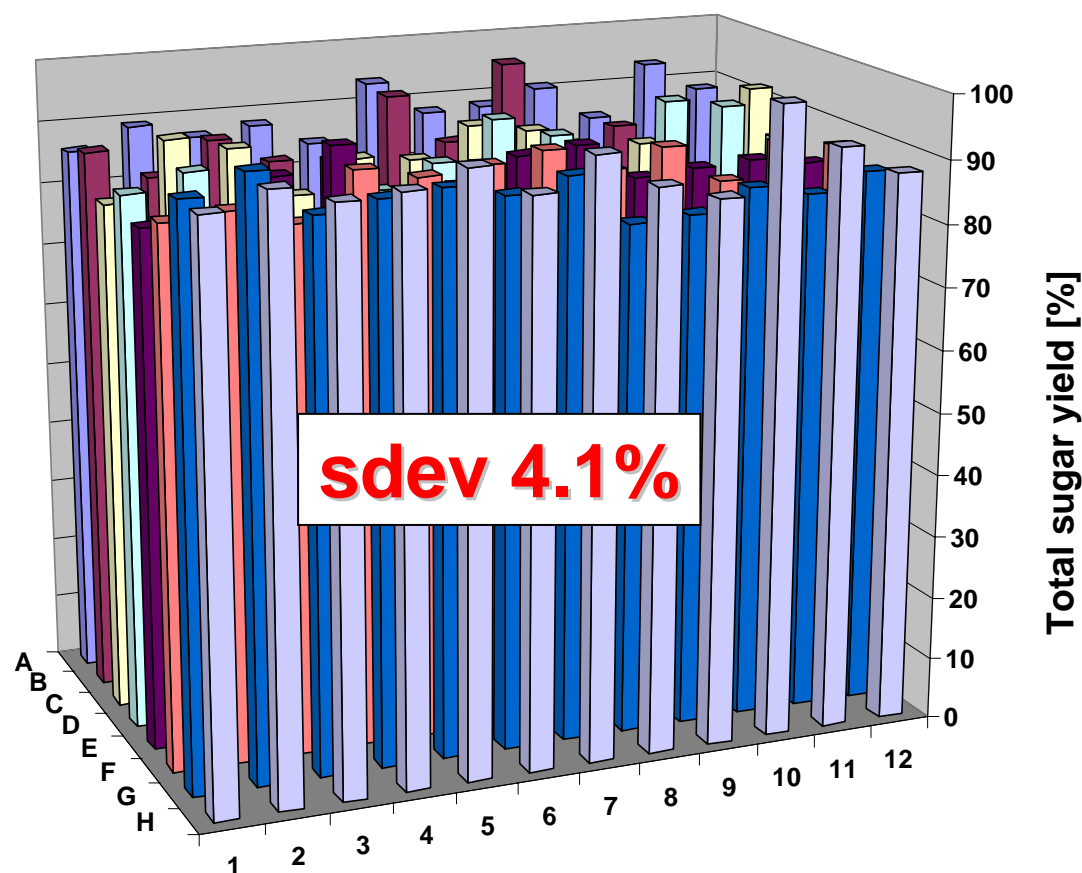


## Unique and Important

- *Steam*: efficient uniform heating
- *No separation*: saves time and increases accuracy
- *2-4mg sample size*: reduces material costs

Studer *et al.*, presented at the 30<sup>th</sup> Symposium  
on Biotechnology for Fuels and Chemicals,  
May 2008

# Proof of Concept: 96 well-plate Pretreatment and Co-hydrolysis Performance



- Poplar (NRELHPT00001)
- Water-only pretreatment at 180°C for 55Min
- 1%w/w solids loading
- Co-hydrolysis: 75 + 25mg of cellulase and xylanase / g of glucan + xylan in the raw biomass
- Heated with steam

# HTP Enzymatic Digestion Assays

- Recalcitrance is ultimately determined by enzyme access to carbohydrates and sugar release
- HTP assays are needed to assess recalcitrant phenotypes and to screen for more effective enzymes
- 1<sup>st</sup> tier assays:
  - >1000 samples/week
    - Evaluate base-line susceptibility of pretreated biomass as well as enzymes from natural diversity
- 2<sup>nd</sup> tier assays: <200 samples/day



Response surface output for multi-dimensional diges

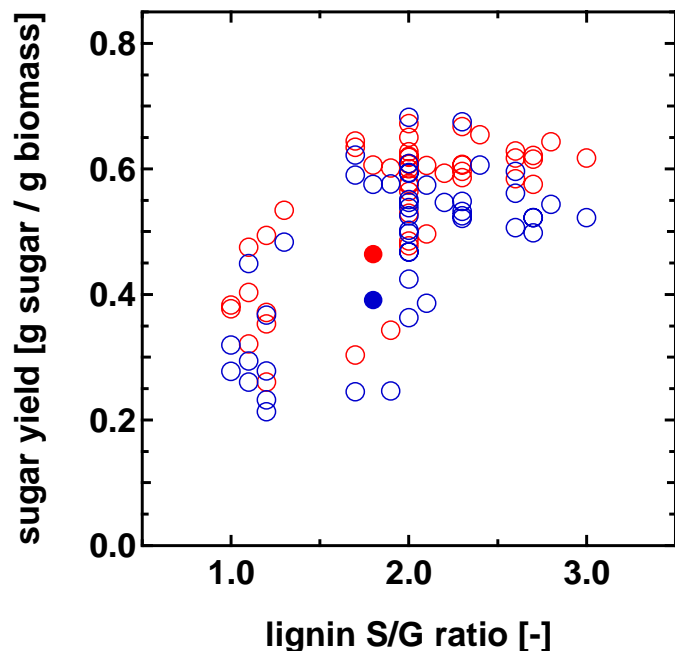
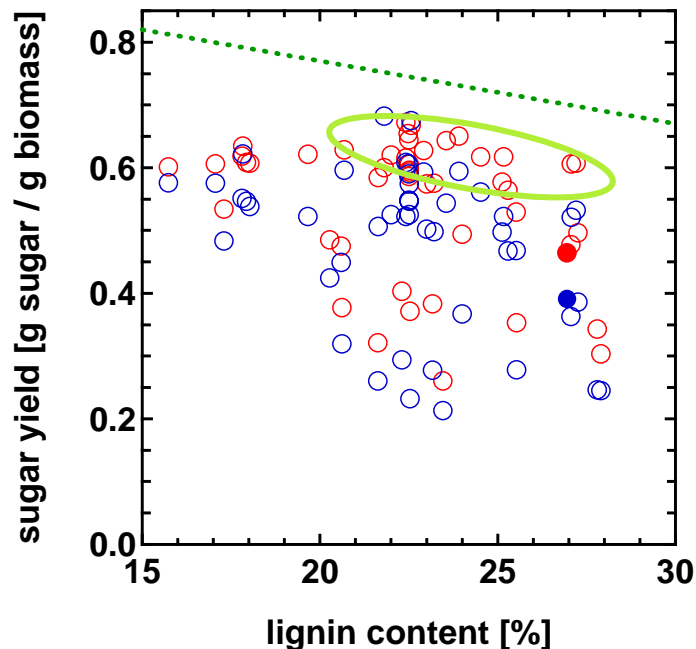
# Populus Association Study

- Tested for enhanced sugar release characteristics through pretreatment and enzymatic hydrolysis
  - Hot water pretreatments at **160** and **180°C**
- HTP pretreatment and co-hydrolysis in 96 well-plates
- Preliminary observations:
  - Sugar yield increases with S/G ratio
  - Lignin content has minimal effect
  - Some outlier poplar samples exhibit very high sugar release
- Characterization pipeline works

Pretreatment conditions: ○ 180°C, 18Min  
○ 160°C, 68Min

● ● Standard BESC poplar

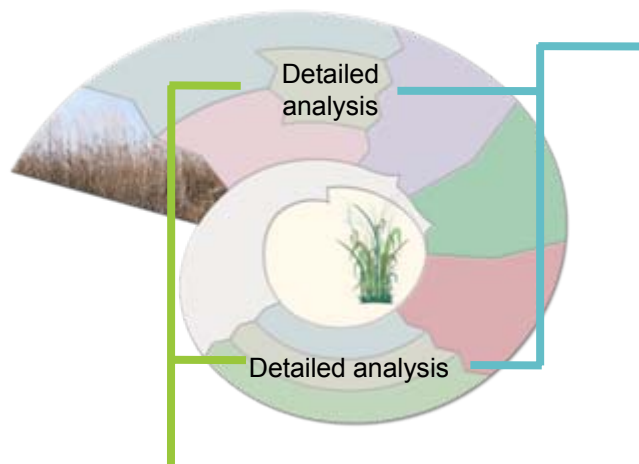
--- Theoretical sugar yield



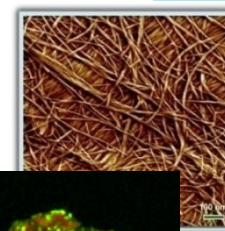


# Detailed Analysis of Specific Samples Inform Cell-wall Chemistry and Structure

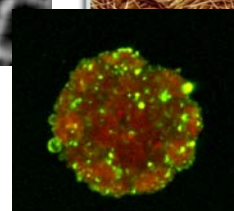
## Imaging



Bio-ultraCAT for  
3-D density of  
*Populus* cell walls

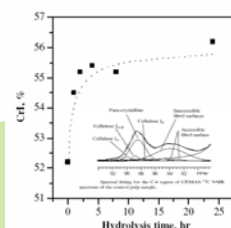


AFM of switchgrass  
showing cellulose  
microfibrils

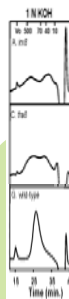


Immunolocalization  
using wall antibodies  
on *Populus* protoplasts

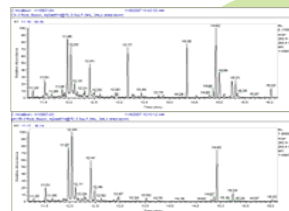
## Chemistry



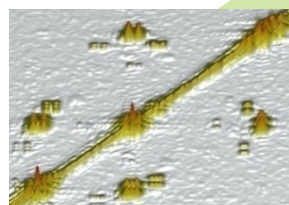
NMR for cellulose  
crystallinity



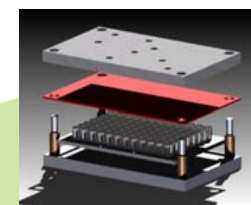
Fractionation and  
chromatography



Mass Spectrometry  
for key metabolites



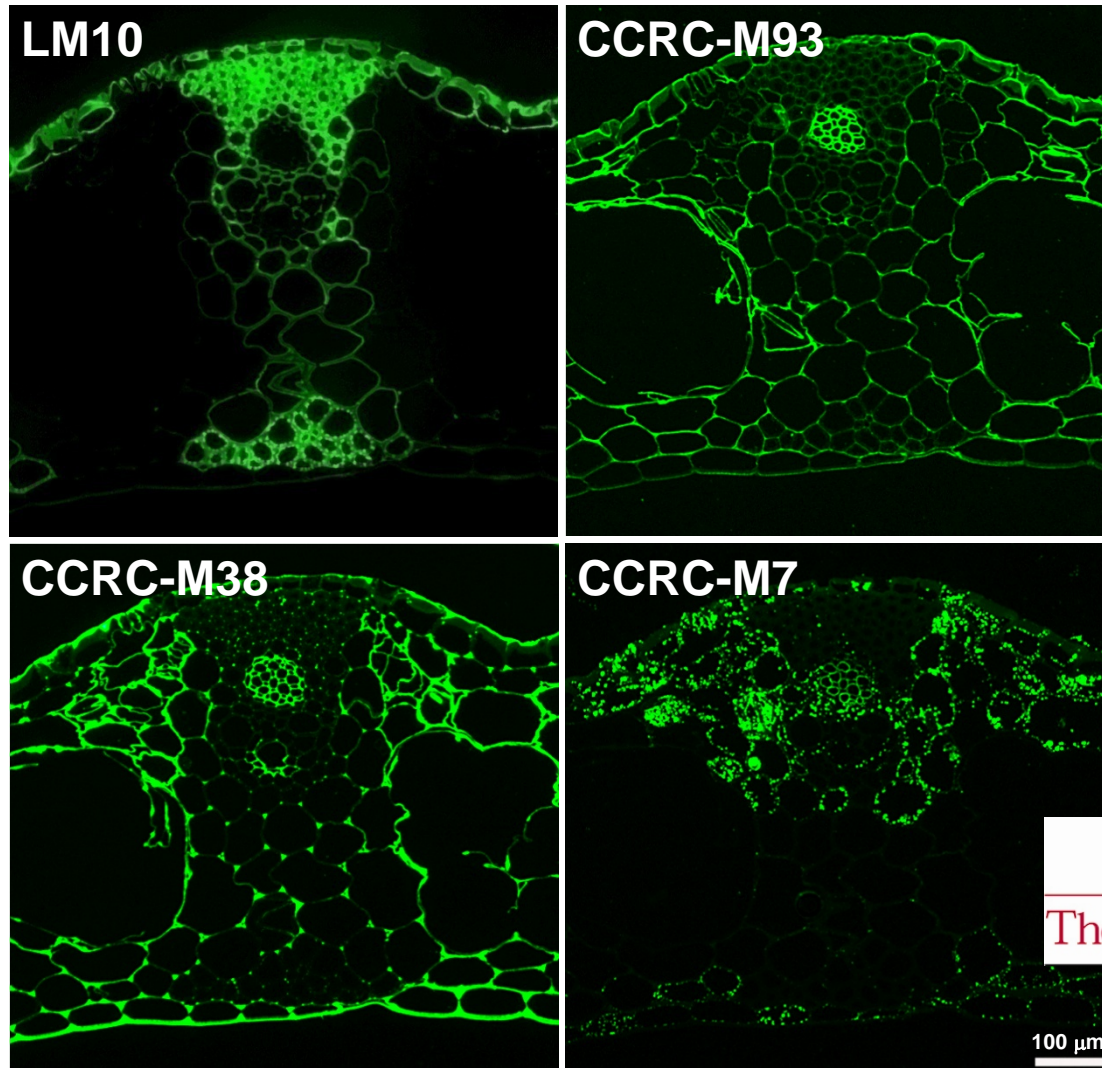
2D <sup>1</sup>H-NMR sees  
altered bonds in  
polysaccharides and  
lignin in biomass



2<sup>nd</sup> tier Enzyme and  
Pretreatment tests

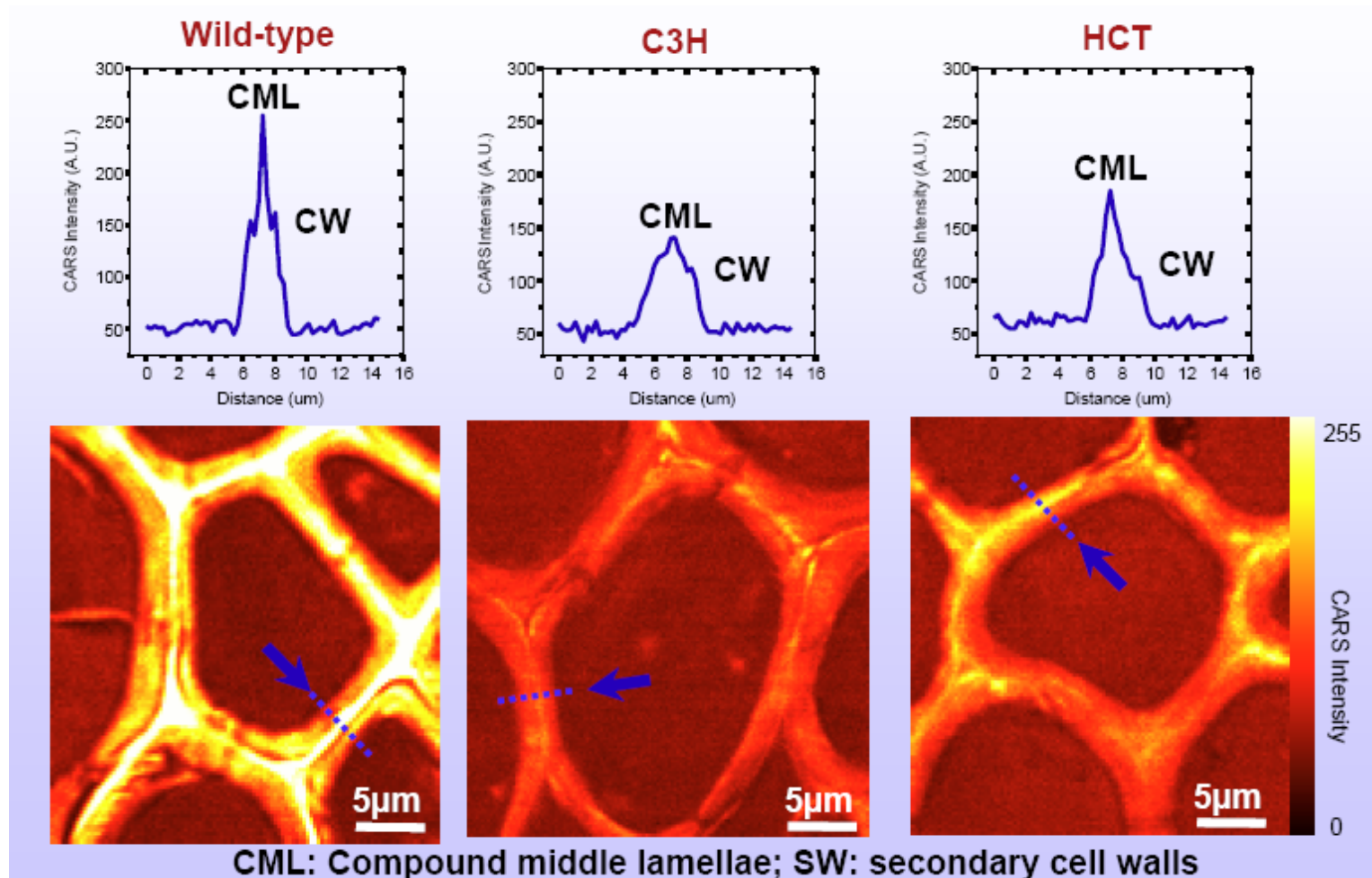
# Immunolocalization of Different Polysaccharide Structures in Leaves of Switchgrass Using Wall-epitope Specific Monoclonal Antibodies

*Utku Avci, Michael Hahn*



The University of Georgia

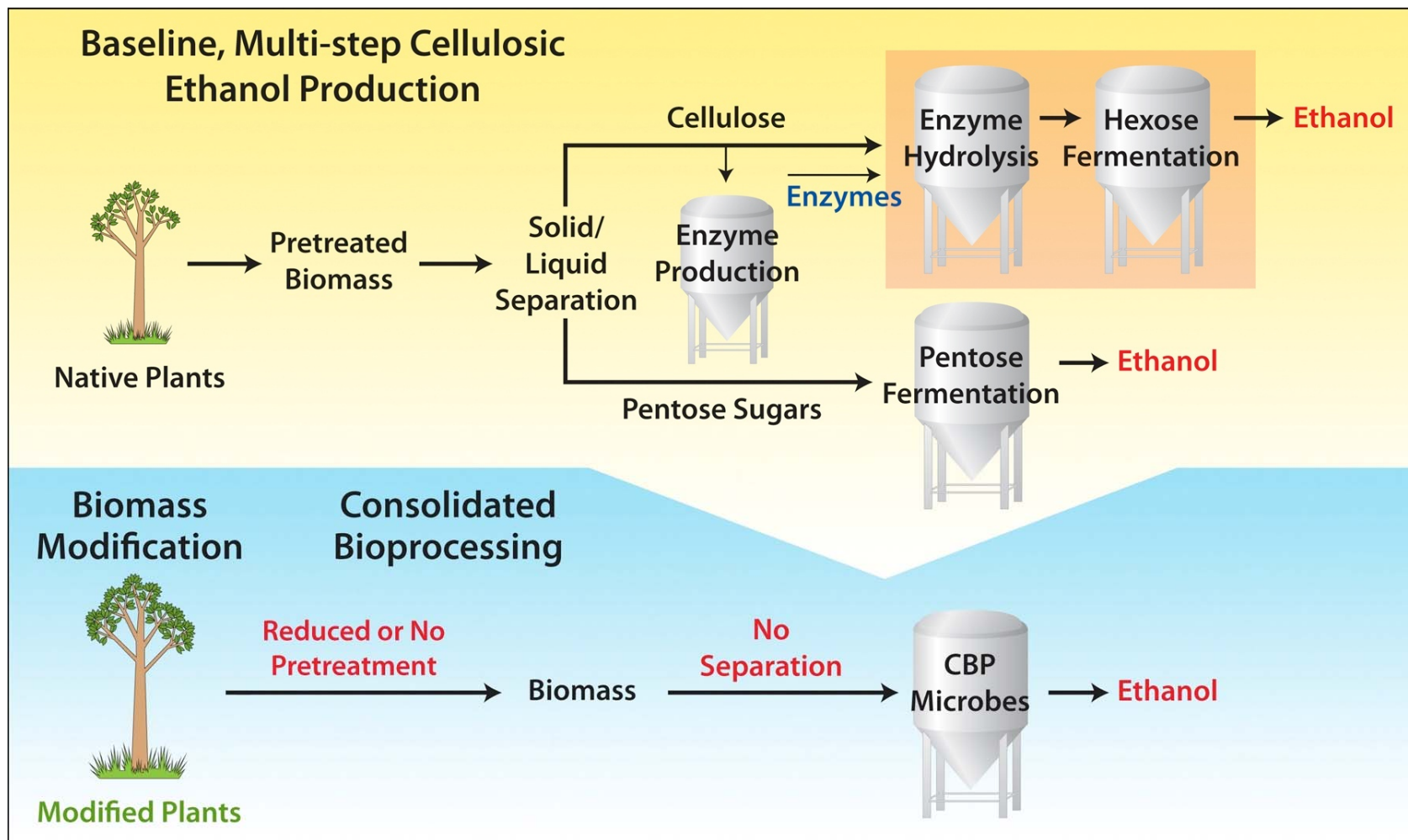
# CARS (Coherent Anti-Stokes Raman Scattering) Imaging of Lignin in Interfascicular Fiber Cell Walls in Alfalfa



S-Y Ding (NREL) and X. S. Xie (Harvard)  
tools under BER imaging grant; sample analysis under BESC, MS in preparation



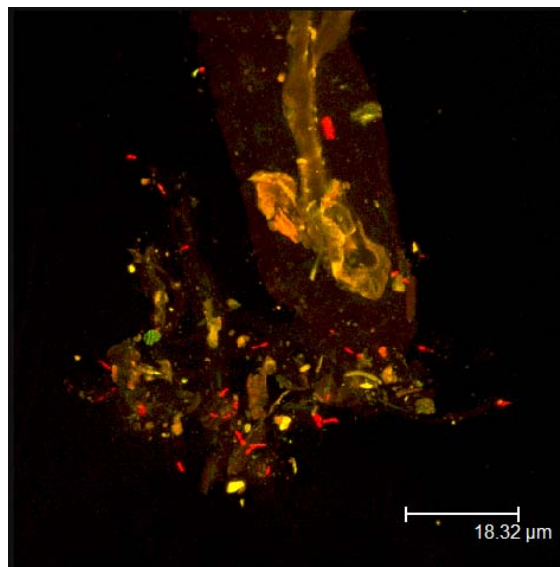
# BESC Will Revolutionize How Biomass is Processed



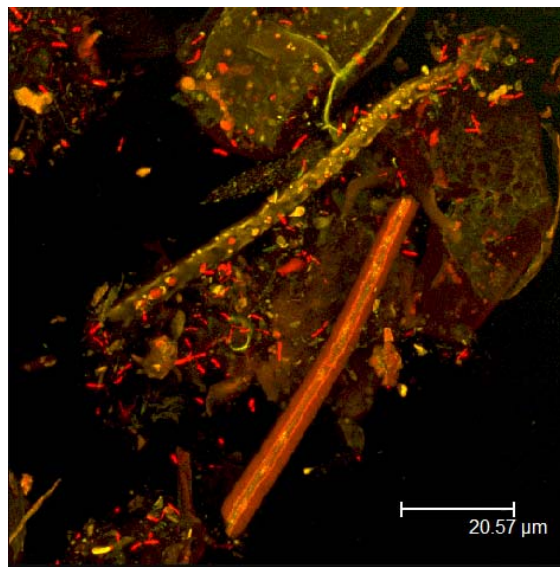


# Temporal Dynamics of *Clostridia thermocellum* Attachment to Pretreated Switchgrass

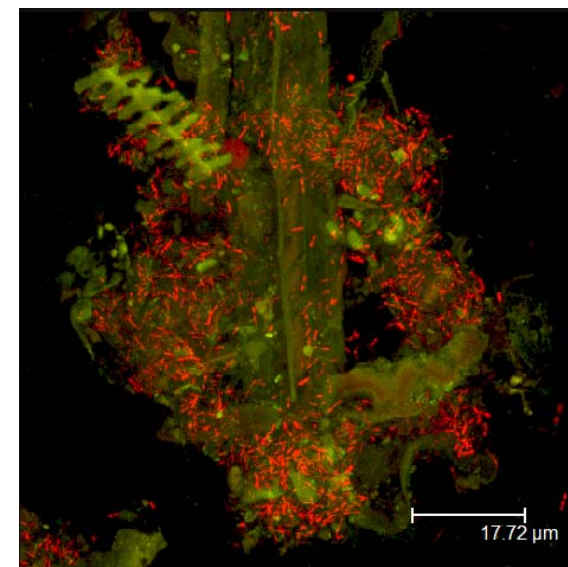
22 h



48 h



113 h



Cells were collected at various timepoints during fermentation, frozen\*, and then stained with Syto9 and Propidium iodide. Z-series optical sections were collected using confocal microscopy and projected as a single 2D image. Overlays of the green (Syto9) and red (PI) channels are shown for each timepoint. Cells provided by B. Raman. \*Since cells were frozen, most stain with PI (dead)

# Thank you Retreat December 2008



**BESC is a U.S. Department of Energy  
Bioenergy Research Center supported by  
the Office of Biological and Environmental  
Research in the DOE Office of Science**





# Highlights 2008-till February 2009



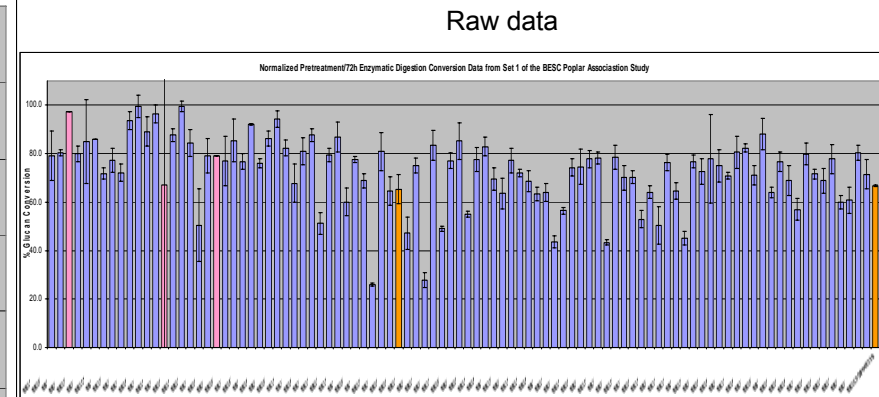
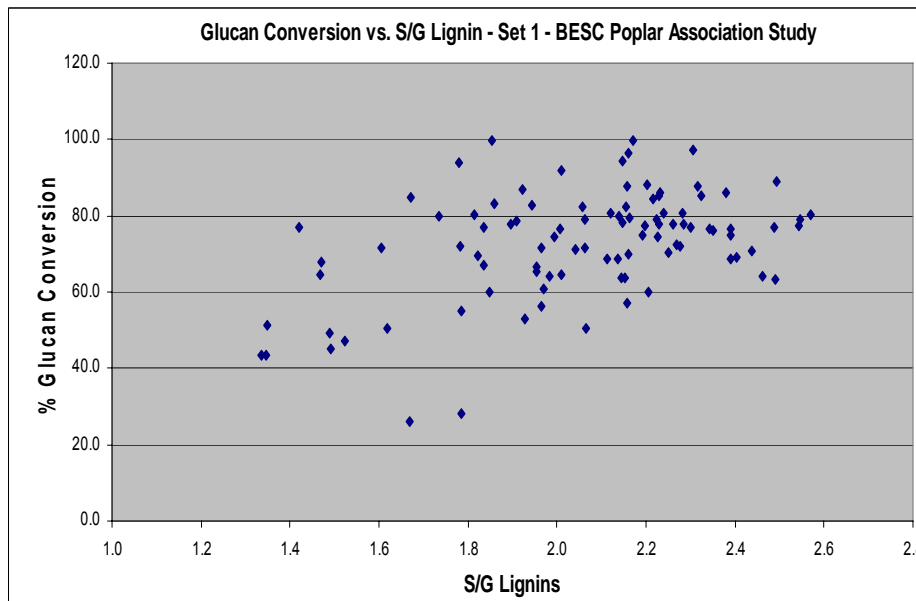
- **138+** Scientific presentations at meetings and conferences worldwide
- **29** Scientific publications
- **11** Workshops and seminars for BESC researchers and graduate students
- **10** Inventions disclosed which are under evaluation by the BESC Commercialization Council and 2 additional in-preparation
- Scientific collaboration with the University of British Columbia has contributed over 250 additional *Populus* samples at no cost to BESC
- **70+** Presentations to Stakeholders (Under Secretaries, Congressmen and Staff Members, Businessmen, etc.)
- **65+** Television, Print, and Radio Interviews
- Education program with the Creative Discovery Museum in Chattanooga, Tennessee to develop a Biofuels Outreach Lesson
- Co-sponsored Global Venture Challenge 2008 in April at ORNL

# HTP Pretreatment/Saccharification Analysis of Poplar Diversity

- **Notes on General Set-Up**

- 95 different samples run in triplicate + stds and controls
- Biomass load at  $5 \pm 0.3$  mg per reactor well
- Pretreatment run at  $180^\circ\text{C}$  for 40 min
- Digestion w 100mg Spezyme/g biomass for 72 h
- Glucose analysis by glucose oxidase assay
- Data normalized to conversion rates for the BESC poplar std

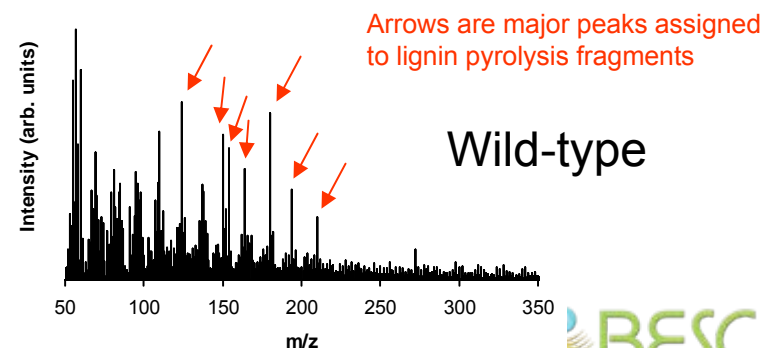
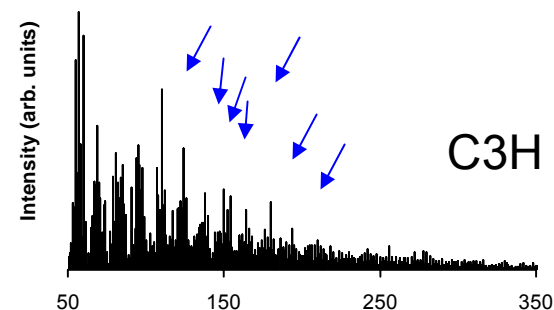
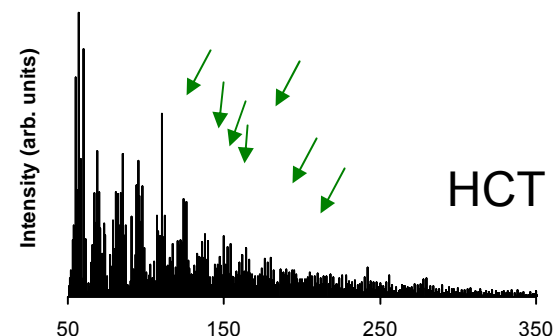
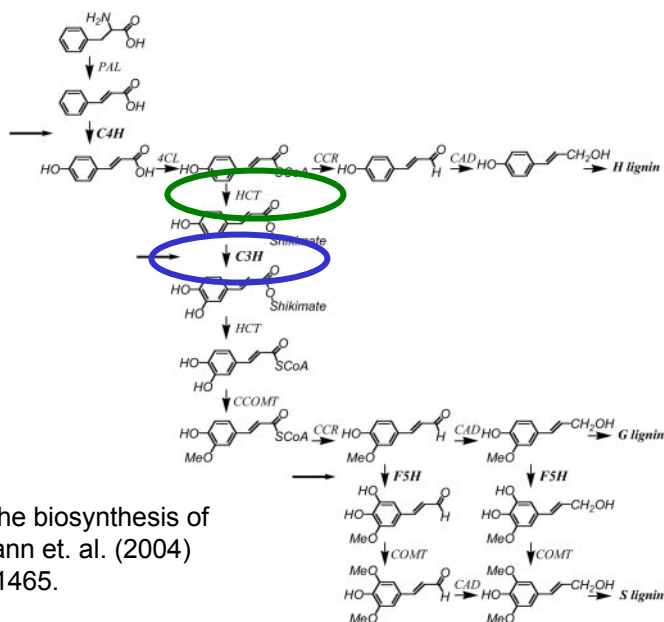
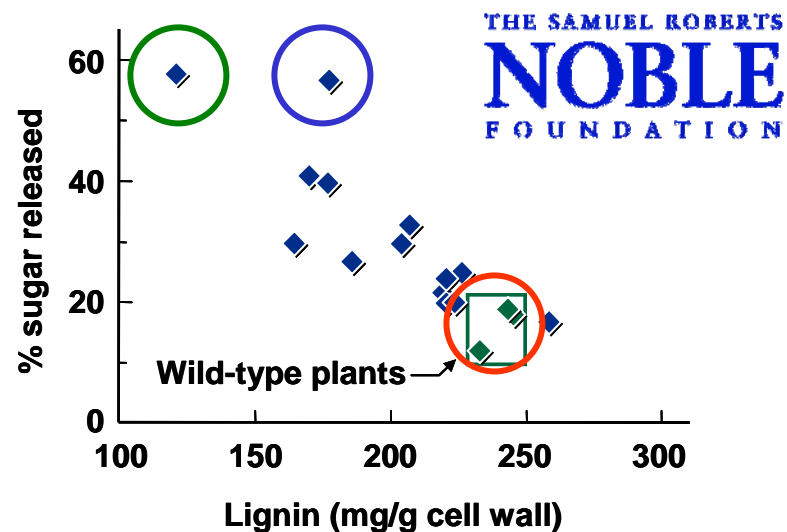
T-test probability  
that groups show  
trend is  $>99.5\%$





# Analytical Pyrolysis of Low Lignin Alfalfa

36 minutes of analysis for 6 (x3) samples

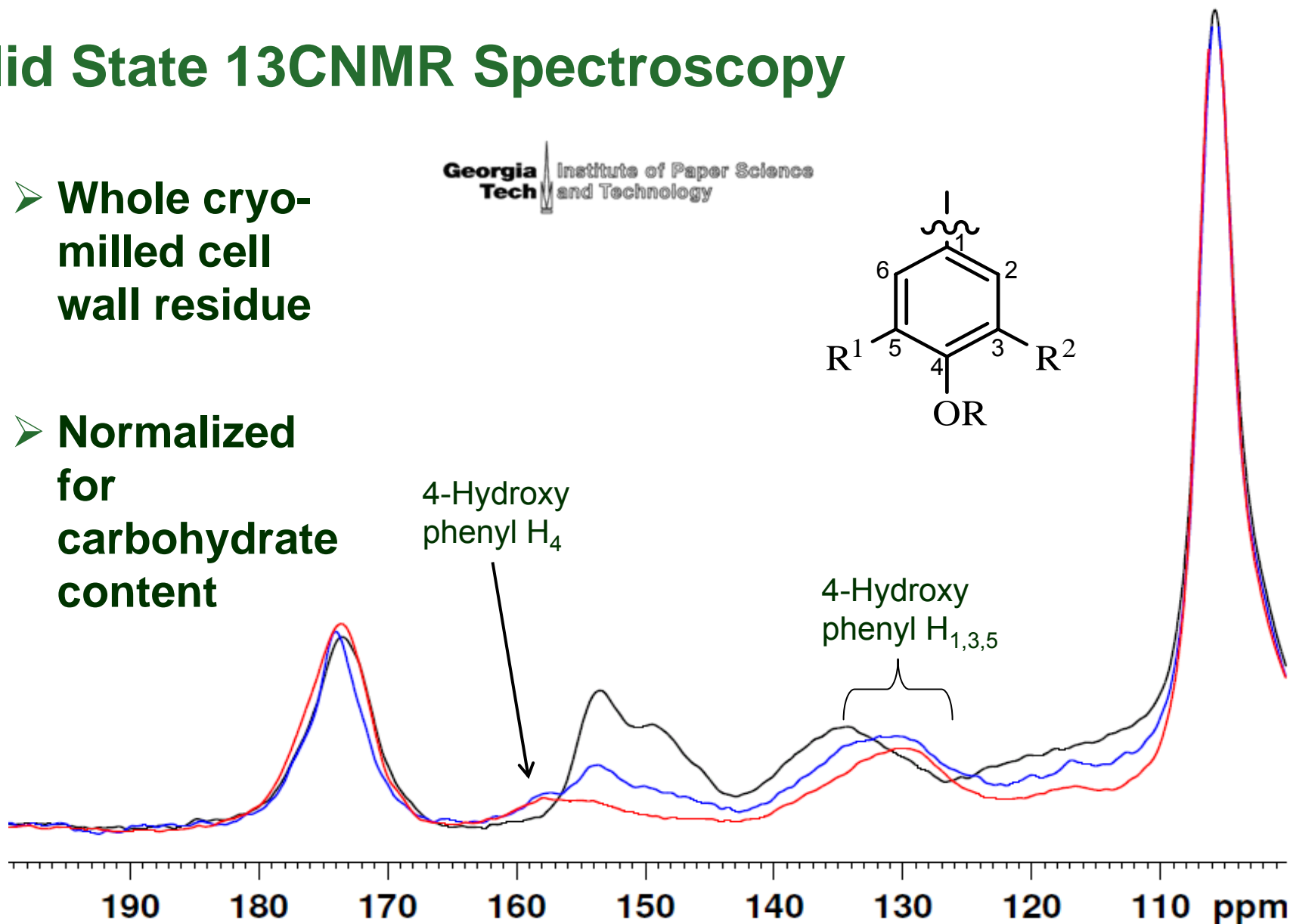
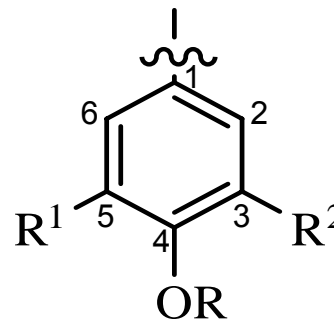


# Solid State $^{13}\text{C}$ NMR Spectroscopy

Georgia Tech Institute of Paper Science and Technology

➤ Whole cryo-milled cell wall residue

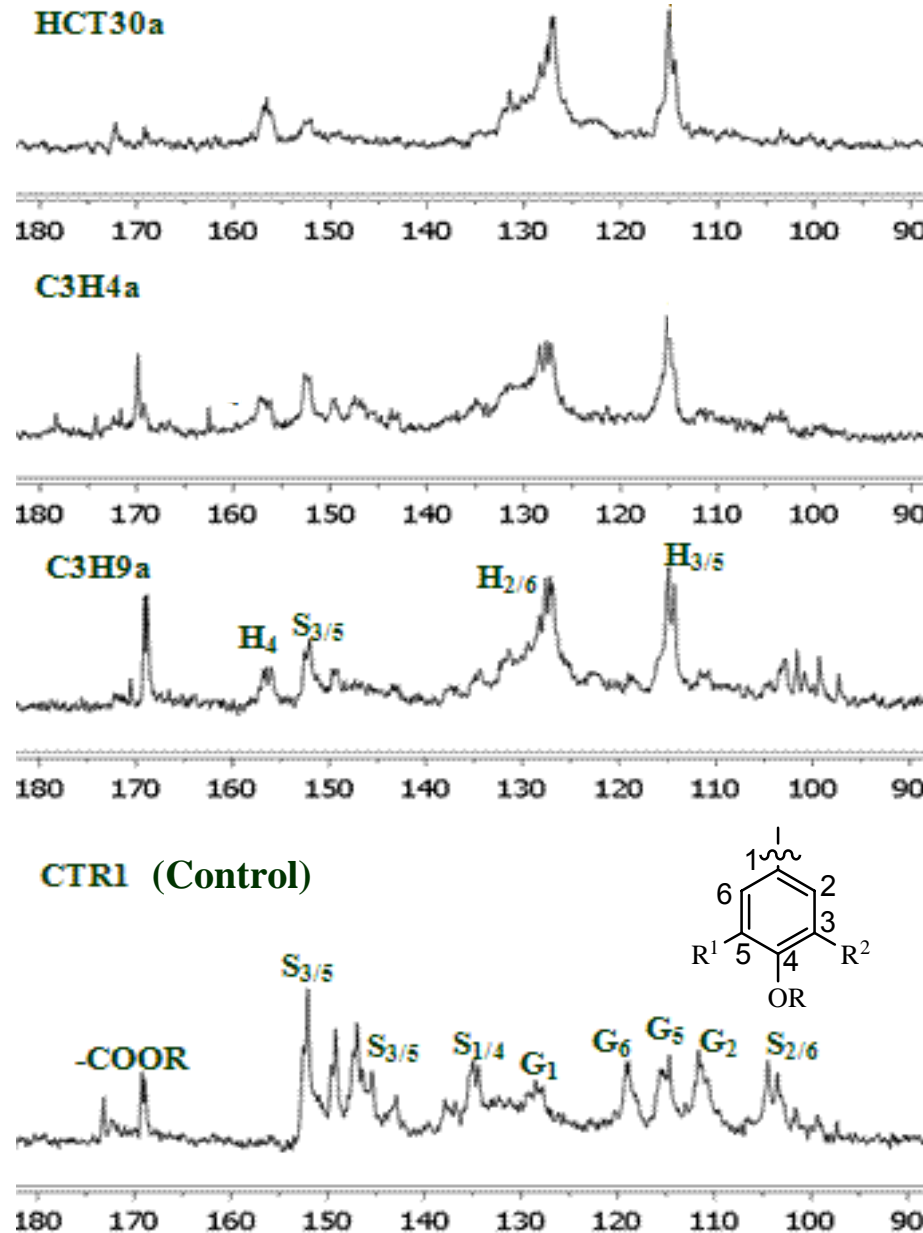
➤ Normalized for carbohydrate content



$^{13}\text{C}$ NMR spectra for the control versus C3H9a and HCT30a

# Quantitative Liquid NMR Spectroscopy

- H lignin peak easily seen in transgenic alfalfa - absent in wild type
- Less S and G lignin



Carbon NMR of ball milled, extracted lignin. HCT30a, C3H4a, C3H9a and Control (CTR1).

# Preliminary Conclusions from Detailed Analysis of Alfalfa Mutants



- Crosslinking between polymers is critical
- Altered localization does occur in mutants
- Crystallinity was not a major factor
- Multiple techniques on same samples add insights in the hands of experts



# Computational Microscope – Assay and Analysis Framework

